

SUPPLEMENTAL MATERIAL

SUPPLEMENTAL FIGURES FOR TEACHING PURPOSES

FIG. S1

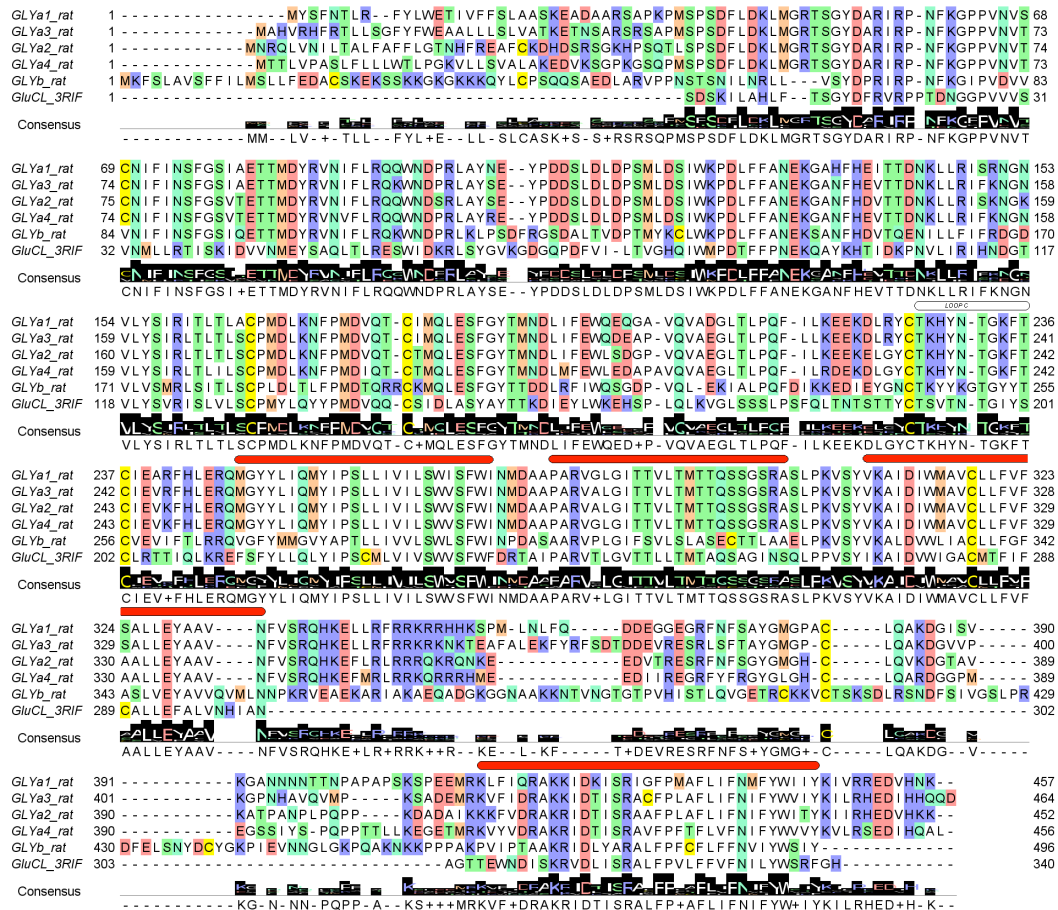


FIGURE S1. Comparison of GlyR subunit sequences with GluC. The sequences of GlyR α 1-4 show a high extent of identity (>80%) as well as significant homology to GluCl, whereas GlyR β is much less conserved. TMs are indicated (red bars), and residues are colour-coded as follows: orange, methionine; yellow, cysteine; green, serine/threonine; cyan, glutamine/asparagine; red, aspartic acid/glutamic acid; blue, histamine/lysine/arginine. The remaining hydrophobic residues are not coloured. A consensus sequence is presented at the bottom.

FIG. S2

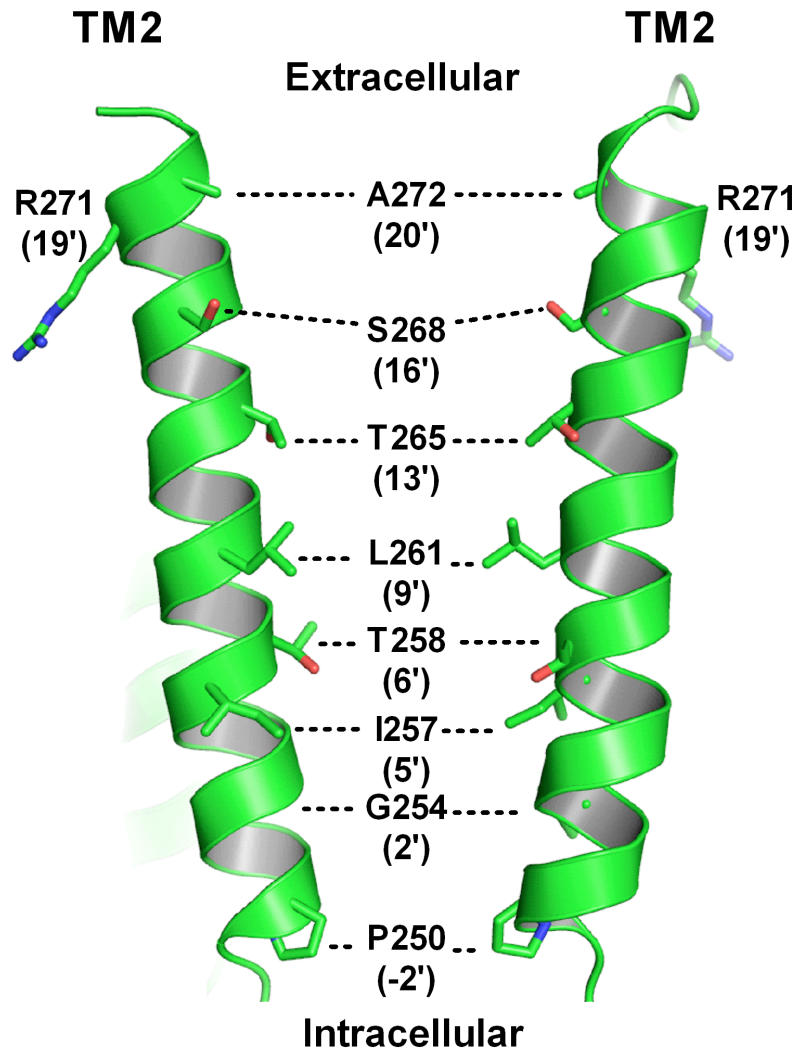


FIGURE S2. **Section through the TM2 regions of the homomeric GlyRα1 channel.** Pore lining residues are indicated. The distance between corresponding residues progressively decreases from the outer (A272; 16.4 Å) to the inner (P250; 8.6 Å) channel mouth. Residue R271, a major site of hyperekplexia mutations, is also shown. The model is based on the open GluCl structure, thus representing the conducting state.